



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Atkinson, John P.
Hourcade, Dennis
Krych, Malgorzata
- (ii) TITLE OF INVENTION: Modified Truncated Complement System
Regulators
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patrea L. Pabst
 - (B) STREET: 2800 One Atlantic Center, 1201 West Peachtree
Street
 - (C) CITY: Atlanta
 - (D) STATE: Georgia
 - (E) COUNTRY: US
 - (F) ZIP: 30309-3450
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/126,505
 - (B) FILING DATE: 24-SEP-1993
 - (C) CLASSIFICATION: 530
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/695,514
 - (B) FILING DATE: 03-MAY-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Pabst, Patrea L.
 - (B) REGISTRATION NUMBER: 31,284
 - (C) REFERENCE/DOCKET NUMBER: WU101CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404) 873-8794
 - (B) TELEFAX: (404) 873-8795

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
 1 5 10 15

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
 20 25 30

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
 35 40 45

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
 1 5 10 15

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
 20 25 30

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
 35 40 45

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CONT.

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 1 5 10 15

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 20 25 30

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 35 40 45

Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Lys Lys Ala Pro Ile Cys Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Asp Pro Leu Pro Glu Cys Arg
 1 5

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cont

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Ser Val Gln
1

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Asp Pro Leu Pro Glu Cys Arg Ser Ser Val Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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Cont.
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Thr Lys Pro Pro Ile Cys Gln Asn Ala Ala His
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Pro Tyr Ile Thr Gln Asn Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Arg Thr Thr Phe His Leu Gly Arg Lys Cys Ser Thr Ala Val Ser
 1 5 10 15

Pro Ala Thr Thr Ser Glu Gly Leu Arg Leu Cys Ala Ala His Pro Arg
 20 25 30

Glu Thr Gly Ala Leu Gln Pro Pro His Val Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..5994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAA TGC AAT GCC CCA GAA TGG CTT CCA TTT GCC AGG CCT ACC AAC CTA 48
 Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

ACT GAT GAG TTT GAG TTT CCC ATT GGG ACA TAT CTG AAC TAT GAA TGC 96
 Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

CGC CCT GGT TAT TCC GGA AGA CCG TTT TCT ATC ATC TGC CTA AAA AAC 144
 Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

TCA GTC TGG ACT GGT GCT AAG GAC AGG TGC AGA CGT AAA TCA TGT CGT 192
 Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

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Cont.

AAT CCT CCA GAT CCT GTG AAT GGC ATG GTG CAT GTG ATC AAA GGC ATC Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile 65 70 75 80	240
CAG TTC GGA TCC CAA ATT AAA TAT TCT TGT ACT AAA GGA TAC CGA CTC Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu 85 90 95	288
ATT GGT TCC TCG TCT GCC ACA TGC ATC ATC TCA GGT GAT ACT GTC ATT Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile 100 105 110	336
TGG GAT AAT GAA ACA CCT ATT TGT GAC AGA ATT CCT TGT GGG CTA CCC Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro 115 120 125	384
CCC ACC ATC ACC AAT GGA GAT TTC ATT AGC ACC AAC AGA GAG AAT TTT Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe 130 135 140	432
CAC TAT GGA TCA GTG GTG ACC TAC CGC TGC AAT CCT GGA AGC GGA GGG His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly 145 150 155 160	480
AGA AAG GTG TTT GAG CTT GTG GGT GAG CCC TCC ATA TAC TGC ACC AGC Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser 165 170 175	528
AAT GAC GAT CAA GTG GGC ATC TGG AGC GGC CCC GCC CCT CAG TGC ATT Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile 180 185 190	576
ATA CCT AAC AAA TGC ACG CCT CCA AAT GTG GAA AAT GGA ATA TTG GTA Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val 195 200 205	624
TCT GAC AAC AGA AGC TTA TTT TCC TTA AAT GAA GTT GTG GAG TTT AGG Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg 210 215 220	672
TGT CAG CCT GGC TTT GTC ATG AAA GGA CCC CGC CGT GTG AAG TGC CAG Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln 225 230 235 240	720
GCC CTG AAC AAA TGG GAG CCG GAG CTA CCA AGC TGC TCC AGG GTA TGT Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys 245 250 255	768
CAG CCA CCT CCA GAT GTC CTG CAT GCT GAG CGT ACC CAA AGG GAC AAG Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys 260 265 270	816
GAC AAC TTT TCA CCT GGG CAG GAA GTG TTC TAC AGC TGT GAG CCC GGC Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly 275 280 285	864
TAC GAC CTC AGA GGG GCT GCG TCT ATG CGC TGC ACA CCC CAG GGA GAC Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp 290 295 300	912

C
Cont.

TGG AGC CCT GCA GCC CCC ACA TGT GAA GTG AAA TCC TGT GAT GAC TTC Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe 305 310 315 320	960
ATG GGC CAA CTT CTT AAT GGC CGT GTG CTA TTT CCA GTA AAT CTC CAG Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln 325 330 335	1008
CTT GGA GCA AAA GTG GAT TTT GTT TGT GAT GAA GGA TTT CAA TTA AAA Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys 340 345 350	1056
GGC AGC TCT GCT AGT TAC TGT GTC TTG GCT GGA ATG GAA AGC CTT TGG Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp 355 360 365	1104
AAT AGC AGT GTT CCA GTG TGT GAA CAA ATC TTT TGT CCA AGT CCT CCA Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro 370 375 380	1152
GTT ATT CCT AAT GGG AGA CAC ACA GGA AAA CCT CTG GAA GTC TTT CCC Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro 385 390 395 400	1200
TTT GGA AAA GCA GTA AAT TAC ACA TGC GAC CCC CAC CCA GAC AGA GGG Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly 405 410 415	1248
ACG AGC TTC GAC CTC ATT GGA GAG AGC ACC ATC CGC TGC ACA AGT GAC Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp 420 425 430	1296
CCT CAA GGG AAT GGG GTT TGG AGC AGC CCT GCC CCT CGC TGT GGA ATT Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile 435 440 445	1344
CTG GGT CAC TGT CAA GCC CCA GAT CAT TTT CTG TTT GCC AAG TTG AAA Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys 450 455 460	1392
ACC CAA ACC AAT GCA TCT GAC TTT CCC ATT GGG ACA TCT TTA AAG TAC Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr 465 470 475 480	1440
GAA TGC CGT CCT GAG TAC TAC GGG AGG CCA TTC TCT ATC ACA TGT CTA Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu 485 490 495	1488
GAT AAC CTG GTC TGG TCA AGT CCC AAA GAT GTC TGT AAA CGT AAA TCA Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser 500 505 510	1536
TGT AAA ACT CCT CCA GAT CCA GTG AAT GGC ATG GTG CAT GTG ATC ACA Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr 515 520 525	1584
GAC ATC CAG GTT GGA TCC AGA ATC AAC TAT TCT TGT ACT ACA GGG CAC Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His 530 535 540	1632

C
Cont.

CGA CTC ATT GGT CAC TCA TCT GCT GAA TGT ATC CTC TCG GGC AAT GCT Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala 545 550 555 560	1680
GCC CAT TGG AGC ACG AAG CCG CCA ATT TGT CAA CGA ATT CCT TGT GGG Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly 565 570 575	1728
CTA CCC CCC ACC ATC GCC AAT GGA GAT TTC ATT AGC ACC AAC AGA GAG Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu 580 585 590	1776
AAT TTT CAC TAT GGA TCA GTG GTG ACC TAC CGC TGC AAT CCT GGA AGC Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser 595 600 605	1824
GGA GGG AGA AAG GTG TTT GAG CTT GTG GGT GAG CCC TCC ATA TAC TGC Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys 610 615 620	1872
ACC AGC AAT GAC GAT CAA GTG GGC ATC TGG AGC GGC CCG GCC CCT CAG Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln 625 630 635 640	1920
TGC ATT ATA CCT AAC AAA TGC ACG CCT CCA AAT GTG GAA AAT GGA ATA Cys Ile Ile Pro Asn Lys Cys Thr Pro Asn Val Glu Asn Gly Ile 645 650 655	1968
TTG GTA TCT GAC AAC AGA AGC TTA TTT TCC TTA AAT GAA GTT GTG GAG Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu 660 665 670	2016
TTT AGG TGT CAG CCT GGC TTT GTC ATG AAA GGA CCC CGC CGT GTG AAG Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys 675 680 685	2064
TGC CAG GCC CTG AAC AAA TGG GAG CCG GAG CTA CCA AGC TGC TCC AGG Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg 690 695 700	2112
GTA TGT CAG CCA CCT CCA GAT GTC CTG CAT GCT GAG CGT ACC CAA AGG Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg 705 710 715 720	2160
GAC AAG GAC AAC TTT TCA CCC GGG CAG GAA GTG TTC TAC AGC TGT GAG Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu 725 730 735	2208
CCC GGC TAT GAC CTC AGA GGG GCT GCG TCT ATG CGC TGC ACA CCC CAG Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln 740 745 750	2256
GGA GAC TGG AGC CCT GCA GCC CCC ACA TGT GAA GTG AAA TCC TGT GAT Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp 755 760 765	2304
GAC TTC ATG GGC CAA CTT CTT AAT GGC CGT GTG CTA TTT CCA GTA AAT Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn 770 775 780	2352

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Cont.

CTC CAG CTT GGA GCA AAA GTG GAT TTT GTT TGT GAT GAA GGA TTT CAA Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln 785 790 795 800	2400
TTA AAA GGC AGC TCT GCT AGT TAT TGT GTC TTG GCT GGA ATG GAA AGC Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser 805 810 815	2448
CTT TGG AAT AGC AGT GTT CCA GTG TGT GAA CAA ATC TTT TGT CCA AGT Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser 820 825 830	2496
CCT CCA GTT ATT CCT AAT GGG AGA CAC ACA GGA AAA CCT CTG GAA GTC Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val 835 840 845	2544
TTT CCC TTT GGA AAA GCA GTA AAT TAC ACA TGC GAC CCC CAC CCA GAC Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp 850 855 860	2592
AGA GGG ACG AGC TTC GAC CTC ATT GGA GAG AGC ACC ATC CGC TGC ACA Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr 865 870 875 880	2640
AGT GAC CCT CAA GGG AAT GGG GTT TGG AGC AGC CCT GCC CCT CGC TGT Ser Asp Pro Gln Gly Asn Val Trp Ser Ser Pro Ala Pro Arg Cys 885 890 895	2688
GGA ATT CTG GGT CAC TGT CAA GCC CCA GAT CAT TTT CTG TTT GCC AAG Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys 900 905 910	2736
TTG AAA ACC CAA ACC AAT GCA TCT GAC TTT CCC ATT GGG ACA TCT TTA Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu 915 920 925	2784
AAG TAC GAA TGC CGT CCT GAG TAC TAC GGG AGG CCA TTC TCT ATC ACA Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr 930 935 940	2832
TGT CTA GAT AAC CTG GTC TGG TCA AGT CCC AAA GAT GTC TGT AAA CGT Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg 945 950 955 960	2880
AAA TCA TGT AAA ACT CCT CCA GAT CCA GTG AAT GGC ATG GTG CAT GTG Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val 965 970 975	2928
ATC ACA GAC ATC CAG GTT GGA TCC AGA ATC AAC TAT TCT TGT ACT ACA Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr 980 985 990	2976
GGG CAC CGA CTC ATT GGT CAC TCA TCT GCT GAA TGT ATC CTC TCA GGC Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly 995 1000 1005	3024
AAT ACT GCC CAT TGG AGC ACG AAG CCG CCA ATT TGT CAA CGA ATT CCT Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro 1010 1015 1020	3072

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Cont

TGT GGG CTA CCC CCA ACC ATC GCC AAT GGA GAT TTC ATT AGC ACC AAC Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn 1025 1030 1035 1040	3120
AGA GAG AAT TTT CAC TAT GGA TCA GTG GTG ACC TAC CGC TGC AAT CTT Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu 1045 1050 1055	3168
GGA AGC AGA GGG AGA AAG GTG TTT GAG CTT GTG GGT GAG CCC TCC ATA Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile 1060 1065 1070	3216
TAC TGC ACC AGC AAT GAC GAT CAA GTG GGC ATC TGG AGC GGC CCC GCC Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala 1075 1080 1085	3264
CCT CAG TGC ATT ATA CCT AAC AAA TGC ACG CCT CCA AAT GTG GAA AAT Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn 1090 1095 1100	3312
GGA ATA TTG GTA TCT GAC AAC AGA AGC TTA TTT TCC TTA AAT GAA GTT Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val 1105 1110 1115 1120	3360
GTG GAG TTT AGG TGT CAG CCT GGC TTT GTC ATG AAA GGA CCC CGC CGT Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg 1125 1130 1135	3408
G TG AAG TGC CAG GCC CTG AAC AAA TGG GAG CCA GAG TTA CCA AGC TGC Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys 1140 1145 1150	3456
TCC AGG GTG TGT CAG CCG CCT CCA GAA ATC CTG CAT GGT GAG CAT ACC Ser Arg Val Cys Gln Pro Pro Glu Ile Leu His Gly Glu His Thr 1155 1160 1165	3504
CCA AGC CAT CAG GAC AAC TTT TCA CCT GGG CAG GAA GTG TTC TAC AGC Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser 1170 1175 1180	3552
TGT GAG CCT GGC TAT GAC CTC AGA GGG GCT GCG TCT CTG CAC TGC ACA Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr 1185 1190 1195 1200	3600
CCC CAG GGA GAC TGG AGC CCT GAA GCC CCG AGA TGT GCA GTG AAA TCC Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser 1205 1210 1215	3648
TGT GAT GAC TTC TTG GGT CAA CTC CCT CAT GGC CGT GTG CTA TTT CCA Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro 1220 1225 1230	3696
CTT AAT CTC CAG CTT GGG GCA AAG GTG TCC TTT GTC TGT GAT GAA GGG Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly 1235 1240 1245	3744
TTT CGC TTA AAG GGC AGT TCC GTT AGT CAT TGT GTC TTG GTT GGA ATG Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met 1250 1255 1260	3792

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Cont.

AGA AGC CTT TGG AAT AAC AGT GTT CCT GTG TGT GAA CAT ATC TTT TGT Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys 1265 1270 1275 1280	3840
CCA AAT CCT CCA GCT ATC CTT AAT GGG AGA CAC ACA GGA ACT CCC TCT Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser 1285 1290 1295	3888
GGA GAT ATT CCC TAT GGA AAA GAA ATA TCT TAC ACA TGT GAC CCC CAC Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His 1300 1305 1310	3936
CCA GAC AGA GGG ATG ACC TTC AAC CTC ATT GGG GAG AGC ACC ATC CGC Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg 1315 1320 1325	3984
TGC ACA AGT GAC CCT CAT GGG AAT GGG GTT TGG AGC AGC CCT GCC CCT Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro 1330 1335 1340	4032
CGC TGT GAA CTT TCT GTT CGT GCT GGT CAC TGT AAA ACC CCA GAG CAG Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln 1345 1350 1355 1360	4080
TTT CCA TTT GCC AGT CCT ACG ATC CCA ATT AAT GAC TTT GAG TTT CCA Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro 1365 1370 1375	4128
GTC GGG ACA TCT TTG AAT TAT GAA TGC CGT CCT GGG TAT TTT GGG AAA Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys 1380 1385 1390	4176
ATG TTC TCT ATC TCC TGC CTA GAA AAC TTG GTC TGG TCA AGT GTT GAA Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu 1395 1400 1405	4224
GAC AAC TGT AGA CGA AAA TCA TGT GGA CCT CCA CCA GAA CCC TTC AAT Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Glu Pro Phe Asn 1410 1415 1420	4272
GGA ATG GTG CAT ATA AAC ACA GAT ACA CAG TTT GGA TCA ACA GTT AAT Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn 1425 1430 1435 1440	4320
TAT TCT TGT AAT GAA GGG TTT CGA CTC ATT GGT TCC CCA TCT ACT ACT Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr 1445 1450 1455	4368
TGT CTC GTC TCA GGC AAT AAT GTC ACA TGG GAT AAG AAG GCA CCT ATT Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile 1460 1465 1470	4416
TGT GAG ATC ATA TCT TGT GAG CCA CCT CCA ACC ATA TCC AAT GGA GAC Cys Glu Ile Ile Ser Cys Glu Pro Pro Thr Ile Ser Asn Gly Asp 1475 1480 1485	4464
TTC TAC AGC AAC AAT AGA ACA TCT TTT CAC AAT GGA ACG GTG GTA ACT Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr 1490 1495 1500	4512

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cont.

TAC CAG TGC CAC ACT GGA CCA GAT GGA GAA CAG CTG TTT GAG CTT GTG Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val 1505 1510 1515 1520	4560
GGA GAA CGG TCA ATA TAT TGC ACC AGC AAA GAT GAT CAA GTT GGT GTT Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val 1525 1530 1535	4608
TGG AGC AGC CCT CCC CCT CGG TGT ATT TCT ACT AAT AAA TGC ACA GCT Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala 1540 1545 1550	4656
CCA GAA GTT GAA AAT GCA ATT AGA GTA CCA GGA AAC AGG AGT TTC TTT Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe 1555 1560 1565	4704
TCC CTC ACT GAG ATC ATC AGA TTT AGA TGT CAG CCC GGG TTT GTC ATG Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met 1570 1575 1580	4752
GTA GGG TCC CAC ACT GTG CAG TGC CAG ACC AAT GGC AGA TGG GGG CCC Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro 1585 1590 1595 1600	4800
AAG CTG CCA CAC TGC TCC AGG GTG TGT CAG CCG CCT CCA GAA ATC CTG Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu 1605 1610 1615	4848
CAT GGT GAG CAT ACC CTA AGC CAT CAG GAC AAC TTT TCA CCT GGG CAG His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln 1620 1625 1630	4896
GAA GTG TTC TAC AGC TGT GAG CCC AGC TAT GAC CTC AGA GGG GCT GCG Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala 1635 1640 1645	4944
TCT CTG CAC TGC ACG CCC CAG GGA GAC TGG AGC CCT GAA GCC CCT AGA Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg 1650 1655 1660	4992
TGT ACA GTG AAA TCC TGT GAT GAC TTC CTG GGC CAA CTC CCT CAT GGC Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly 1665 1670 1675 1680	5040
CGT GTG CTA CTT CCA CTT AAT CTC CAG CTT GGG GCA AAG GTG TCC TTT Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe 1685 1690 1695	5088
GTT TGC GAT GAA GGG TTC CGA TTA AAA GGC AGG TCT GCT AGT CAT TGT Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys 1700 1705 1710	5136
GTC TTG GCT GGA ATG AAA GCC CTT TGG AAT AGC AGT GTT CCA GTG TGT Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys 1715 1720 1725	5184
GAA CAA ATC TTT TGT CCA AAT CCT CCA GCT ATC CTT AAT GGG AGA CAC Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His 1730 1735 1740	5232

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Cont.

ACA GGA ACT CCC TTT GGA GAT ATT CCC TAT GGA AAA GAA ATA TCT TAC Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr 1745 1750 1755 1760	5280
GCA TGC GAC ACC CAC CCA GAC AGA GGG ATG ACC TTC AAC CTC ATT GGG Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly 1765 1770 1775	5328
GAG AGC TCC ATC CGC TGC ACA AGT GAC CCT CAA GGG AAT GGG GTT TGG Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp 1780 1785 1790	5376
AGC AGC CCT GCC CCT CGC TGT GAA CTT TCT GTT CCT GCT GCC TGC CCA Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro 1795 1800 1805	5424
CAT CCA CCC AAG ATC CAA AAC GGG CAT TAC ATT GGA GGA CAC GTA TCT His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser 1810 1815 1820	5472
CTA TAT CTT CCT GGG ATG ACA ATC AGC TAC ACT TGT GAC CCC GGC TAC Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr 1825 1830 1835 1840	5520
CTG TTA GTG GGA AAG GGC TTC ATT TTC TGT ACA GAC CAG GGA ATC TGG Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp 1845 1850 1855	5568
AGC CAA TTG GAT CAT TAT TGC AAA GAA GTA AAT TGT AGC TTC CCA CTG Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu 1860 1865 1870	5616
TTT ATG AAT GGA ATC TCG AAG GAG TTA GAA ATG AAA AAA GTA TAT CAC Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His 1875 1880 1885	5664
TAT GGA GAT TAT GTG ACT TTG AAG TGT GAA GAT GGG TAT ACT CTG GAA Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu 1890 1895 1900	5712
GGC AGT CCC TGG AGC CAG TGC CAG GCG GAT GAC AGA TGG GAC CCT CCT Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro 1905 1910 1915 1920	5760
CTG GCC AAA TGT ACC TCT CGT GCA CAT GAT GCT CTC ATA GTT GGC ACT Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val Gly Thr 1925 1930 1935	5808
TTA TCT GGT ACG ATC TTC TTT ATT TTA CTC ATC ATT TTC CTC TCT TGG Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu Ser Trp 1940 1945 1950	5856
ATA ATT CTA AAG CAC AGA AAA GGC AAT AAT GCA CAT GAA AAC CCT AAA Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn Pro Lys 1955 1960 1965	5904
GAA GTG GCT ATC CAT TTA CAT TCT CAA GGA GGC AGC AGC GTT CAT CCC Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val His Pro 1970 1975 1980	5952

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Cont

CGA ACT CTG CAA ACA AAT GAA GAA AAT AGC AGG GTC CTT CCT Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro 1985 1990 1995	5994
TGACAAAGTA CTATACAGCT GAAGAACATC TCGAATACAA TTTTGGTGGG AAAGGAGCCA	6054
ATTGATTCAGCA ACAGAACATCAG ATCTGAGCTT CATAAAAGTCT TTGAAGTGAC TTCACAGAGA	6114
CGCAGACATG TGCACITGAA GATGCTGCC CTTCCCTGGT ACCTAGCAAA GCTCCTGCCT	6174
CTTTGTGTGC GTCACTGTGA AACCCCCACC CTTCTGCCTC GTGCTAAACG CACACAGTAT	6234
CTAGTCAGGG GAAAAGACTG CATTAGGAG ATAGAAAATA GTTTGGATTA CTTAAAGGAA	6294
TAAGGTGTTG CCTGGAATTCTGGTTGTA AGGTGGTCAC TGTTCTTTT TAAAATATT	6354
GTAATATGGA ATGGGCTCAG TAAGAAGAGC TTGGAAAATG CAGAAAGTTA TGAAAATAA	6414
GTCACCTATA ATTATGCTAC CTACTGATAA CCACTCCTAA TATTTTGATT CATTTCCTGC	6474
CTATCTCTT TCACATATGT GTTTTTTAC ATACGTACTT TTCCCCCTT AGTTTGTTC	6534
CTTTTATTTT ATAGAGCAGA ACCCTAGTCT TTTAACAGT TTAGAGTGAA ATATATGCTA	6594
TATCAGTTTT TACTTCTCT AGGGAGAAAA ATTAATTTAC TAGAAAGGCA TGAAATGATC	6654
ATGGGAAGAG TGGTTAAGAC TACTGAAGAG AAATATTTGG AAAATAAGAT TTCGATATCT	6714
TCTTTTTTTTGAGATGGAG TCTGGCTCTG TCTCCAGGC TGGAGTGCAG TGGCGTAATC	6774
TCGGCTCACT GCAACGTCCG CCTCCCG	6801

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1998 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Cont.

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu 1 5 10 15
Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys 20 25 30
Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn 35 40 45
Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg 50 55 60
Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile 65 70 75 80
Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110
 Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125
 Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140
 His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350
 Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

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Cont.

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
 515 520 525

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640

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Cont.
 Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 1010 1015 1020

Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 1025 1030 1035 1040

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu
 1045 1050 1055

Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 1060 1065 1070

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 1075 1080 1085

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 1090 1095 1100

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 Cont.

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 1105 1110 1115 1120

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
 1125 1130 1135

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 1140 1145 1150

Ser Arg Val Cys Gln Pro Pro Glu Ile Leu His Gly Glu His Thr
 1155 1160 1165

Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 1170 1175 1180

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr
 1185 1190 1195 1200

Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser
 1205 1210 1215

Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro
 1220 1225 1230

Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly
 1235 1240 1245

Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met
 1250 1255 1260

Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys
 1265 1270 1275 1280

Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser
 1285 1290 1295

Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His
 1300 1305 1310

Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg
 1315 1320 1325

Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 1330 1335 1340

Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln
 1345 1350 1355 1360

Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro
 1365 1370 1375

Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys
 1380 1385 1390

Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu
 1395 1400 1405

Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Glu Pro Phe Asn
 1410 1415 1420

Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn
 1425 1430 1435 1440

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Cont.

Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr
 1445 1450 1455
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile
 1460 1465 1470
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp
 1475 1480 1485
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr,
 1490 1495 1500
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val
 1505 1510 1515 1520
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val
 1525 1530 1535
 Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
 1540 1545 1550
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe
 1555 1560 1565
 Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met
 1570 1575 1580
 Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro
 1585 1590 1595 1600
 Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu
 1605 1610 1615
 His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln
 1620 1625 1630
 Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala
 1635 1640 1645
 Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg
 1650 1655 1660
 Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly
 1665 1670 1675 1680
 Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe
 1685 1690 1695
 Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys
 1700 1705 1710
 Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys
 1715 1720 1725
 Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His
 1730 1735 1740
 Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr
 1745 1750 1755 1760
 Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly
 1765 1770 1775

Cont.

Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
 1780 1785 1790
 Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro
 1795 1800 1805
 His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser
 1810 1815 1820
 Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr
 1825 1830 1835 1840
 Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp
 1845 1850 1855
 Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu
 1860 1865 1870
 Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His
 1875 1880 1885
 Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu
 1890 1895 1900
 Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro
 1905 1910 1915 1920
 Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val Gly Thr
 1925 1930 1935
 Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu Ser Trp
 1940 1945 1950
 Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn Pro Lys
 1955 1960 1965
 Glu Val Ala Ile His Leu His Ser Gln Gly Ser Ser Val His Pro
 1970 1975 1980
 Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro
 1985 1990 1995

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3036 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

C
Cont.

ATT TCT TGT GGC TCT CCT CCG CCT ATC CTA AAT GGC CGG ATT AGT TAT Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr 1 5 10 15	48
TAT TCT ACC CCC ATT GCT GTT GGT ACC GTG ATA AGG TAC AGT TGT TCA Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser 20 25 30	96
GGT ACC TTC CGC CTC ATT GGA GAA AAA AGT CTA TTA TGC ATA ACT AAA Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys 35 40 45	144
GAC AAA GTG GAT GGA ACC TGG GAT AAA CCT GCT CCT AAA TGT GAA TAT Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr 50 55 60	192
TTC AAT AAA TAT TCT TCT TGC CCT GAG CCC ATA GTA CCA GGA GGA TAC Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr 65 70 75 80	240
AAA ATT AGA GGC TCT ACA CCC TAC AGA CAT GGT GAT TCT GTG ACA TTT Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe 85 90 95	288
GCC TGT AAA ACC AAC TTC TCC ATG AAC GGA AAC AAG TCT GTT TGG TGT Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys 100 105 110	336
CAA GCA AAT AAT ATG TGG GGG CCG ACA CGA CTA CCA ACC TGT GTA AGT Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser 115 120 125	384
GTT TTC CCT CTC GAG TGT CCA GCA CTT CCT ATG ATC CAC AAT GGA CAT Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His 130 135 140	432
CAC ACA AGT GAG AAT GTT GGC TCC ATT GCT CCA GGA TTG TCT GTG ACT His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr 145 150 155 160	480
TAC AGC TGT GAA TCT GGT TAC TTG CTT GTT GGA GAA AAG ATC ATT AAC Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn 165 170 175	528
TGT TTG TCT TCG GGA AAA TGG AGT GCT GTC CCC CCC ACA TGT GAA GAG Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu 180 185 190	576
GCA CGC TGT AAA TCT CTA GGA CGA TTT CCC AAT GGG AAG GTA AAG GAG Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu 195 200 205	624
CCT CCA ATT CTC CGG GTT GGT GTA ACT GCA AAC TTT TTC TGT GAT GAA Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu 210 215 220	672
GGG TAT CGA CTG CAA GGC CCA CCT TCT AGT CGG TGT GTA ATT GCT GGA Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly 225 230 235 240	720

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Cont.

CAG GGA GTT GCT TGG ACC AAA ATG CCA GTA TGT GAA GAA ATT TTT TGC Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu Glu Ile Phe Cys 245 250 255	768
CCA TCA CCT CCC CCT ATT CTC AAT GGA AGA CAT ATA GGC AAC TCA CTA Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile Gly Asn Ser Leu 260 265 270	816
GCA AAT GTC TCA TAT GGA AGC ATA GTC ACT TAC ACT TGT GAC CCG GAC Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr Cys Asp Pro Asp 275 280 285	864
CCA GAG GAA GGA GTG AAC TTC ATC CTT ATT GGA GAG AGC ACT CTC CGT Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu Ser Thr Leu Arg 290 295 300	912
TGT ACA GTT GAT AGT CAG AAG ACT GGG ACC TGG AGT GGC CCT GCC CCA Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser Gly Pro Ala Pro 305 310 315 320	960
CGC TGT GAA CTT TCT ACT TCT GCG GTT CAG TGT CCA CAT CCC CAG ATC Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro His Pro Gln Ile 325 330 335	1008
CTA AGA GGC CGA ATG GTA TCT GGG CAG AAA GAT CGA TAT ACC TAT AAC Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg Tyr Thr Tyr Asn 340 345 350	1056
GAC ACT GTG ATA TTT GCT TGC ATG TTT GGC TTC ACC TTG AAG GGC AGC Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr Leu Lys Gly Ser 355 360 365	1104
AAG CAA ATC CGA TGC AAT GCC CAA GGC ACA TGG GAG CCA TCT GCA CCA Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu Pro Ser Ala Pro 370 375 380	1152
GTC TGT GAA AAG GAA TGC CAG GCC CCT CCT AAC ATC CTC AAT GGG CAA Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile Leu Asn Gly Gln 385 390 395 400	1200
AAG GAA GAT AGA CAC ATG GTC CGC TTT GAC CCT GGA ACA TCT ATA AAA Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly Thr Ser Ile Lys 405 410 415	1248
TAT AGC TGT AAC CCT GGC TAT GTG CTG GTG GGA GAA GAA TCC ATA CAG Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu Glu Ser Ile Gln 420 425 430	1296
TGT ACC TCT GAG GTG TGG ACA CCC CCT GTA CCC CAA TGC AAA GTG GCA Cys Thr Ser Glu Val Trp Thr Pro Pro Val Pro Gln Cys Lys Val Ala 435 440 445	1344
GCG TGT GAA GCT ACA GGA AGG CAA CTC TTG ACA AAA CCC CAG CAC CAA Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr Lys Pro Gln His Gln 450 455 460	1392
TTT GTT AGA CCA GAT GTC AAC TCT TCT TGT GGT GAA GGG TAC AAG TTA Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly Glu Gly Tyr Lys Leu 465 470 475 480	1440

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CONT.

AGT GGG AGT GTT TAT CAG GAG TGT CAA GGC ACA ATT CCT TGG TTT ATG Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr Ile Pro Trp Phe Met 485 490 495	1488
GAG ATT CGT CTT TGT AAA GAA ATC ACC TGC CCA CCA CCC CCT GTT ATC Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro Pro Pro Val Ile 500 505 510	1536
TAC AAT GGG GCA CAC ACC GGG AGT TCC TTA GAA GAT TTT CCA TAT GGA Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu Asp Phe Pro Tyr Gly 515 520 525	1584
ACC ACG GTC ACT TAC ACA TGT AAC CCT GGG CCA GAA AGA GGA GTG GAA Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro Glu Arg Gly Val Glu 530 535 540	1632
TTC AGC CTC ATT GGA GAG AGC ACC ATC CGT TGT ACA AGC AAT GAT CAA Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asn Asp Gln 545 550 555 560	1680
GAA AGA GGC ACC TGG AGT GGC CCT GCT CCC CTG TGT AAA CTT TCC CTC Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu Cys Lys Leu Ser Leu 565 570 575	1728
CTT GCT GTC CAG TGC TCA CAT GTC CAT ATT GCA AAT GGA TAC AAG ATA Leu Ala Val Gln Cys Ser His Val His Ile Ala Asn Gly Tyr Lys Ile 580 585 590	1776
TCT GGC AAG GAA GCC CCA TAT TTC TAC AAT GAC ACT GTG ACA TTC AAG Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp Thr Val Thr Phe Lys 595 600 605	1824
TGT TAT AGT GGA TTT ACT TTG AAG GGC AGT AGT CAG ATT CGT TGC AAA Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser Gln Ile Arg Cys Lys 610 615 620	1872
GCT GAT AAC ACC TGG GAT CCT GAA ATA CCA GTT TGT GAA AAA GAA ACA Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val Cys Glu Lys Glu Thr 625 630 635 640	1920
TGC CAG CAT GTG AGA CAG AGT CTT CAA GAA CTT CCA GCT GGT TCA CGT Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu Pro Ala Gly Ser Arg 645 650 655	1968
GTG GAG CTA GTT AAT ACG TCC TGC CAA GAT GGG TAC CAG TTG ACT GGA Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly Tyr Gln Leu Thr Gly 660 665 670	2016
CAT GCT TAT CAG ATG TGT CAA GAT GCT GAA AAT GGA ATT TGG TTC AAA His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn Gly Ile Trp Phe Lys 675 680 685	2064
AAG ATT CCA CTT TGT AAA GTT ATT CAC TGT CAC CCT CCA CCA GTG ATT Lys Ile Pro Leu Cys Lys Val Ile His Cys His Pro Pro Pro Val Ile 690 695 700	2112
GTC AAT GGG AAG CAC ACA GGC ATG ATG GCA GAA AAC TTT CTA TAT GGA Val Asn Gly Lys His Thr Gly Met Met Ala Glu Asn Phe Leu Tyr Gly 705 710 715 720	2160

C
Cont.

AAT GAA GTC TCT TAT GAA TGT GAC CAA GGA TTC TAT CTC CTG GGA GAG Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe Tyr Leu Leu Gly Glu 725 730 735	2208
AAA AAA TTG CAG TGC AGA AGT GAT TCT AAA GGA CAT GGA TCT TGG AGC Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly His Gly Ser Trp Ser 740 745 750	2256
GGG CCT TCC CCA CAG TGC TTA CGA TCT CCT CCT GTG ACT CGC TGC CCT Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro Val Thr Arg Cys Pro 755 760 765	2304
AAT CCA GAA GTC AAA CAT GGG TAC AAG CTC AAT AAA ACA CAT TCT GCA Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala 770 775 780	2352
TAT TCC CAC AAT GAC ATA GTG TAT GTT GAC TGC AAT CCT GGC TTC ATC Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys Asn Pro Gly Phe Ile 785 790 795 800	2400
ATG AAT GGT AGT CGC GTG ATT AGG TGT CAT ACT GAT AAC ACA TGG GTG Met Asn Gly Ser Arg Val Ile Arg Cys His Thr Asp Asn Thr Trp Val 805 810 815	2448
CCA GGT GTG CCA ACT TGT ATC AAA AAA GCC TTC ATA GGG TGT CCA CCT Pro Gly Val Pro Thr Cys Ile Lys Ala Phe Ile Gly Cys Pro Pro 820 825 830	2496
CCG CCT AAG ACC CCT AAC GGG AAC CAT ACT GGT GGA AAC ATA GCT CGA Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly Gly Asn Ile Ala Arg 835 840 845	2544
TTT TCT CCT GGA ATG TCA ATC CTG TAC AGC TGT GAC CAA GGC TAC CTG Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys Asp Gln Gly Tyr Leu 850 855 860	2592
CTG GTG GGA GAG GCA CTC CTT CTT TGC ACA CAT GAG GGA ACC TGG AGC Leu Val Gly Ala Leu Leu Cys Thr His Glu Gly Thr Trp Ser 865 870 875 880	2640
CAA CCT GCC CCT CAT TGT AAA GAG GTA AAC TGT AGC TCA CCA GCA GAT Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys Ser Ser Pro Ala Asp 885 890 895	2688
ATG GAT GGA ATC CAG AAA GGG CTG GAA CCA AGG AAA ATG TAT CAG TAT Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg Lys Met Tyr Gln Tyr 900 905 910	2736
GGA GCT GTT GTA ACT CTG GAG TGT GAA GAT GGG TAT ATG CTG GAA GGC Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly Tyr Met Leu Glu Gly 915 920 925	2784
AGT CCC CAG AGC CAG TGC CAA TCG GAT CAC CAA TGG AAC CCT CCC CTG Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln Trp Asn Pro Pro Leu 930 935 940	2832
GCG GTT TGC AGA TCC CGT TCA CTT GCT CCT GTC CTT TGT GGT ATT GCT Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val Leu Cys Gly Ile Ala 945 950 955 960	2880

C
Cont.

GCA GGT TTG ATA CTT CTT ACC TTC TTG ATT GTC GTT ACC TTA TAC GTG Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val Val Thr Leu Tyr Val 965 970 975	2928
ATA TCA AAA CAC AGA GCA CGC AAT TAT TAT ACA GAT ACA AGC CAG AAA Ile Ser Lys His Arg Ala Arg Asn Tyr Tyr Thr Asp Thr Ser Gln Lys 980 985 990	2976
GAA GCT TTT CAT TTA GAA GCA CGA GAA GTA TAT TCT GTT GAT CCA TAC Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr Ser Val Asp Pro Tyr 995 1000 1005	3024
AAC CCA GCC AGC Asn Pro Ala Ser 1010	3036

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1012 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
1 5 10 15

Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
20 25 30

Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
35 40 45

Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
50 55 60

Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65 70 75 80

Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
85 90 95

Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
100 105 110

Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
115 120 125

Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
130 135 140

His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145 150 155 160

Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
165 170 175

C
Cont

Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
 180 185 190
 Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
 195 200 205
 Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
 210 215 220
 Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
 225 230 235 240
 Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu Glu Ile Phe Cys
 245 250 255
 Pro Ser Pro Pro Ile Leu Asn Gly Arg His Ile Gly Asn Ser Leu
 260 265 270
 Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr Cys Asp Pro Asp
 275 280 285
 Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu Ser Thr Leu Arg
 290 295 300
 Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser Gly Pro Ala Pro
 305 310 315 320
 Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro His Pro Gln Ile
 325 330 335
 Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg Tyr Thr Tyr Asn
 340 345 350
 Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr Leu Lys Gly Ser
 355 360 365
 Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu Pro Ser Ala Pro
 370 375 380
 Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile Leu Asn Gly Gln
 385 390 395 400
 Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly Thr Ser Ile Lys
 405 410 415
 Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu Glu Ser Ile Gln
 420 425 430
 Cys Thr Ser Glu Val Trp Thr Pro Pro Val Pro Gln Cys Lys Val Ala
 435 440 445
 Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr Lys Pro Gln His Gln
 450 455 460
 Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly Glu Gly Tyr Lys Leu
 465 470 475 480
 Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr Ile Pro Trp Phe Met
 485 490 495
 Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro Pro Pro Val Ile
 500 505 510

C
Cont.

Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu Asp Phe Pro Tyr Gly
 515 520 525
 Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro Glu Arg Gly Val Glu
 530 535 540
 Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asn Asp Gln
 545 550 555 560
 Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu Cys Lys Leu Ser Leu
 565 570 575
 Leu Ala Val Gln Cys Ser His Val His Ile Ala Asn Gly Tyr Lys Ile
 580 585 590
 Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp Thr Val Thr Phe Lys
 595 600 605
 Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser Gln Ile Arg Cys Lys
 610 615 620
 Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val Cys Glu Lys Glu Thr
 625 630 635 640
 Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu Pro Ala Gly Ser Arg
 645 650 655
 Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly Tyr Gln Leu Thr Gly
 660 665 670
 His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn Gly Ile Trp Phe Lys
 675 680 685
 Lys Ile Pro Leu Cys Lys Val Ile His Cys His Pro Pro Pro Val Ile
 690 695 700
 Val Asn Gly Lys His Thr Gly Met Met Ala Glu Asn Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro Val Thr Arg Cys Pro
 755 760 765
 Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys Asn Pro Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser Arg Val Ile Arg Cys His Thr Asp Asn Thr Trp Val
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Lys Lys Ala Phe Ile Gly Cys Pro Pro
 820 825 830
 Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly Gly Asn Ile Ala Arg
 835 840 845

C
Cont.

Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys Asp Gln Gly Tyr Leu
 850 855 860
 Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys Ser Ser Pro Ala Asp
 885 890 895
 Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg Lys Met Tyr Gln Tyr
 900 905 910
 Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly Tyr Met Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val Leu Cys Gly Ile Ala
 945 950 955 960
 Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val Val Thr Leu Tyr Val
 965 970 975
 Ile Ser Lys His Arg Ala Arg Asn Tyr Tyr Thr Asp Thr Ser Gln Lys
 980 985 990
 Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr Ser Val Asp Pro Tyr
 995 1000 1005
 Asn Pro Ala Ser
 1010

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAC TGT GGC CTT CCC CCA GAT GTA CCT AAT GCC CAG CCA GCT TTG GAA 48
 Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1 5 10 15

GGC CGT ACA AGT TTT CCC GAG GAT ACT GTA ATA ACG TAC AAA TGT GAA 96
 Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
 20 25 30

GAA AGC TTT GTG AAA ATT CCT GGC GAG AAG GAC TCA GTG ACC TGC CTT 144
 Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Thr Cys Leu
 35 40 45

C
Cont

AAG GGC ATG CAA TGG TCA GAT ATT GAA GAG TTC TGC AAT CGT AGC TGC Lys Gly Met Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys 50 55 60	192
GAG GTG CCA ACA AGG CTA AAT TCT GCA TCC CTC AAA CAG CCT TAT ATC Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile 65 70 75 80	240
ACT CAG AAT TAT TTT CCA GTC GGT ACT GTT GTG GAA TAT GAG TGC CGT Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg 85 90 95	288
CCA GGT TAC AGA AGA GAA CCT TCT CTA TCA CCA AAA CTA ACT TGC CTT Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu 100 105 110	336
CAG AAT TTA AAA TGG TCC ACA GCA GTC GAA TTT TGT AAA AAG AAA TCA Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Ser 115 120 125	384
TGC CCT AAT CCG GGA GAA ATA CGA AAT GGT CAG ATT GAT GTA CCA GGT Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly 130 135 140	432
GGC ATA TTA TTT GGT GCA ACC ATC TCC TTC TCA TGT AAC ACA GGG TAC Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr 145 150 155 160	480
AAA TTA TTT GGC TCG ACT TCT AGT TTT TGT CTT ATT TCA GGC AGC TCT Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser 165 170 175	528
GTC CAG TGG AGT GAC CCG TTG CCA GAG TGC AGA GAA ATT TAT TGT CCA Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro 180 185 190	576
GCA CCA CCA CAA ATT GAC AAT GGA ATA ATT CAA GGG GAA CGT GAC CAT Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His 195 200 205	624
TAT GGA TAT AGA CAG TCT GTA ACG TAT GCA TGT AAT AAA GGA TTC ACC Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr 210 215 220	672
ATG ATT GGA GAG CAC TCT ATT TAT TGT ACT GTG AAT AAT GAT GAA GGA Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly 225 230 235 240	720
GAG TGG AGT GGC CCA CCA CCT GAA TGC AGA GGA AAA TCT CTA ACT TCC Glu Trp Ser Gly Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser 245 250 255	768
AAG GTC CCA CCA ACA GTT CAG AAA CCT ACC ACA GTA AAT GTT CCA ACT Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr 260 265 270	816
ACA GAA GTC TCA CCA ACT TCT CAG AAA ACC ACC ACA AAA ACC ACC ACA Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Lys Thr Thr Thr 275 280 285	864

C
Cont.

CCA AAT GCT CAA GCA ACA CGG AGT ACA CCT GTT TCC AGG ACA ACC AAG Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys 290 295 300	912
CAT TTT CAT GAA ACA ACC CCA AAT AAA GGA AGT GGA ACC ACT TCA GGT His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly 305 310 315 320	960
ACT ACC CGT CTT CTA TCT GGG CAC ACG TGT TTC ACG TTG ACA GGT TTG Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu 325 330 335	1008
CTT GGG ACG CTA GTA ACC ATG GGC TTG CTG ACT TAGCCAAAGA AGAGTTAAGA Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr 340 345	1061
AGAAAATACA CACAAGTATA CAGACTGTTCTAGTTTCTT AGACTTATCT GCATATTGGA TAAAATAAAT GCAATTGTGC TCTTCATTAA GGATGCTTTC ATTGTCTTTA AGATGTGTTA GGAATGTCAA CAGAGCAAGG AGAAAAAAGG CAGTCCTGGA ATCACATTCT TAGCACACCT GCGCCTCTTG AAAATAGAAC AACTTGCAGA ATTGAGAGTG ATTCCCTTCC TAAAAGTGTAA AGAAAGCATA GAGATTGTT CGTATTAAGA ATGGGATCAC GAGGAAAAGA GAAGGAAAGT GATTTTTTTC CACAAGATCT GAAATGATAT TTCCACTTAT AAAGGAAATA AAAAATGAAA AACATTATTT GGATATCAAA AGCAAATAAA AACCCAATTG AGTCTCTTCT AAGCAAAATT GCTAAAGAGA GATGACCACA TTATAAAGTA ATCTTTGGCT AAGGCATTTC CATCTTCCT TCGGTTGGCA AAATATTTTA AAGGTAAAAC ATGCTGGTGA ACCAGGGTGT TGATGGTGAT AAGGGAGGAA TATAGAATGA AAGACTGAAT CTTCCCTTGT TGCACAAATA GAGTTTGGAA AAAGCCTGTG AAAGGTGTCT TCTTTGACTT AATGTCTTTA AAAGTATCCA GAGATACTAC AATATTAACA TAAGAAAAGA TTATATATTA TTTCTGAATC GAGATGTCCA TAGTCAAATT TGTAATCTT ATTCTTTGT AATATTTATT TATATTTATT TATGACAGTG AACATTCTGA TTTACATGT AAAACAAGAA AAGTTGAAGA AGATATGTGA AGAAAAATGT ATTTTCCTA AATAGAAATA AATGATCCCATTTTTGTT	1121 1181 1241 1301 1361 1421 1481 1541 1601 1661 1721 1781 1841 1901 1930

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu	
1 5 10 15	

C
Cont

Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
 20 25 30

Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Thr Cys Leu
 35 40 45

Lys Gly Met Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
 50 55 60

Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
 65 70 75 80

Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
 85 90 95

Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
 100 105 110

Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser
 115 120 125

Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
 130 135 140

Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
 145 150 155 160

Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
 165 170 175

Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
 180 185 190

Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
 195 200 205

Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
 210 215 220

Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
 225 230 235 240

Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser
 245 250 255

Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro Thr
 260 265 270

Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr
 275 280 285

Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr Lys
 290 295 300

His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly
 305 310 315 320

Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu
 325 330 335

Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
 340 345

1
Cont.

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1050 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGT GAG GAG CCA CCA ACA TTT GAA GCT ATG GAG CTC ATT GGT AAA CCA	48
Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro	
1 5 10 15	
AAA CCC TAC TAT GAG ATT GGT GAA CGA GTA GAT TAT AAG TGT AAA AAA	96
Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys	
20 25 30	
GGA TAC TTC TAT ATA CCT CCT CTT GCC ACC CAT ACT ATT TGT GAT CGG	144
Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg	
35 40 45	
AAT CAT ACA TGG CTA CCT GTC TCA GAT GAC GCC TGT TAT AGA GAA ACA	192
Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr	
50 55 60	
TGT CCA TAT ATA CGG GAT CCT TTA AAT GGC CAA GCA GTC CCT GCA AAT	240
Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro Ala Asn	
65 70 75 80	
GGG ACT TAC GAG TTT GGT TAT CAG ATG CAC TTT ATT TGT AAT GAG GGT	288
Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly	
85 90 95	
TAT TAC TTA ATT GGT GAA GAA ATT CTA TAT TGT GAA CTT AAA GGA TCA	336
Tyr Tyr Leu Ile Gly Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser	
100 105 110	
GTA GCA ATT TGG AGC GGT AAG CCC CCA ATA TGT GAA AAG GTT TTG TGT	384
Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys	
115 120 125	
ACA CCA CCT CCA AAA ATA AAA AAT GGA AAA CAC ACC TTT AGT GAA GTA	432
Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val	
130 135 140	
GAA GTA TTT GAG TAT CTT GAT GCA GTA ACT TAT AGT TGT GAT CCT GCA	480
Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp Pro Ala	
145 150 155 160	
CCT GGA CCA GAT CCA TTT TCA CTT ATT GGA GAG AGC ACG ATT TAT TGT	528
Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys	
165 170 175	

C
Cont.

GGT GAC AAT TCA GTG TGG AGT CGT GCT GCT CCA GAG TGT AAA GTG GTC Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val 180 185 190	576
AAA TGT CGA TTT CCA GTA GTC GAA AAT GGA AAA CAG ATA TCA GGA TTT Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe 195 200 205	624
GGA AAA AAA TTT TAC TAC AAA GCA ACA GTT ATG TTT GAA TGC GAT AAG Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys 210 215 220	672
GGT TTT TAC CTC GAT GGC AGC GAC ACA ATT GTC TGT GAC AGT AAC AGT Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser 225 230 235 240	720
ACT TGG GAT CCC CCA GTT CCA AAG TGT CTT AAA GTG TCG ACT TCT TCC Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr Ser Ser 245 250 255	768
ACT ACA AAA TCT CCA GCG TCC AGT GCC TCA GGT CCT AGG CCT ACT TAC Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro Thr Tyr 260 265 270	816
AAG CCT CCA GTC TCA AAT TAT CCA GGA TAT CCT AAA CCT GAG GAA GGA Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu Glu Gly 275 280 285	864
ATA CTT GAC AGT TTG GAT GTT TGG GTC ATT GCT GTG ATT GTT ATT GCC Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val Ile Ala 290 295 300	912
ATA GTT GTT GGA GTT GCA GTA ATT TGT GTT GTC CCG TAC AGA TAT CTT Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg Tyr Leu 305 310 315 320	960
CAA AGG AGG AAG AAG AAA GGG AAA GCA GAT GGT GGA GCT GAA TAT GCC Gln Arg Arg Lys Lys Lys Gly Lys Ala Asp Gly Gly Ala Glu Tyr Ala 325 330 335	1008
ACT TAC CAG ACT AAA TCA ACC ACT CCA GCA GAG CAG AGA GGC Thr Tyr Gln Thr Lys Ser Thr Pro Ala Glu Gln Arg Gly 340 345 350	1050

(2) INFORMATION FOR SEQ ID NO:19:

- , (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro 1 5 10 15
Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys 20 25 30

C
CONT

Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg
 35 40 45

Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr
 50 55 60

Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro Ala Asn
 65 70 75 80

Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly
 85 90 95

Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser
 100 105 110

Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys
 115 120 125

Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val
 130 135 140

Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp Pro Ala
 145 150 155 160

Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys
 165 170 175

Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val
 180 185 190

Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe
 195 200 205

Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys
 210 215 220

Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser
 225 230 235 240

Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr Ser Ser
 245 250 255

Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro Thr Tyr
 260 265 270

Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu Glu Gly
 275 280 285

Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val Ile Ala
 290 295 300

Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg Tyr Leu
 305 310 315 320

Gln Arg Arg Lys Lys Lys Gly Lys Ala Asp Gly Gly Ala Glu Tyr Ala
 325 330 335

Thr Tyr Gln Thr Lys Ser Thr Thr Pro Ala Glu Gln Arg Gly
 340 345 350

C
Cont